

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANTS: Chatterjee, Deb K.
Solus, Joseph
Yang, Shuwei
- (ii) TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 93
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
(B) STREET: 1100 New York Ave., N.W., Suite 600
(C) CITY: Washington
15 (D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: (To be assigned)
25 (B) FILING DATE: 06-FEB-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: (To be assigned)
(B) FILING DATE: 06-JAN-1998
(C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/037,393
(B) FILING DATE: 07-FEB-1997
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0942.4250002
- (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2682 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

5

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATGGCGAGAC TATTTCTCTT TGATGGCACA GCCCTGGCCT ACAGGGCATA TTACGCCCTC	60
	GACAGATCCC TTTCACATC CACAGGAATT CCAACGAACG CCGTCTATGG CGTTGCCAGG	120
10	ATGCTCGTTA AATTTCATTAA GGAACACATT ATACCCGAAA AGGACTACGC GGCTGTGGCC	180
	TTTGACAAGA AGGCAGCGAC GTTCAGACAC AAAGTGTCTG TAAGCGACAA GGCAGCAAGG	240
	CCTAAGACTC CGGCTCTTCT AGTTTCAGCAG CTACCTTACA TCAAGCGGCT GATAGAAGCT	300
	CTTGGTTTCA AAGTGTCTGA GCTGGAGGGA TACGAAGCAG ACGATATCAT CGCCACGCTT	360
	GCAGTCAGGG CTGCACGTTT TTTGATGAGA TTTTCATTAA TAACCGGTGA CAAGGATATG	420
15	CTTCAACTTG TAAACGAGAA GATAAAGGTC TGGAGAATCG TCAAGGGGAT ATCGGATCTT	480
	GAGCTTTACG ATTTCGAAAA GGTGAAAGAA AGATACGGTG TGAACCCACA TCAGATACCG	540
	GATCTTCTAG CACTGACGGG AGACGACATA GACAACATTC CCGGTGTAA CCGGAATAGGT	600
	GAAAAGACCG CTGTACAGCT TCTCGGCAAG TATAGAAATC TTGAATACAT TCTGGAGCAT	660
	GCCCGTGAAC TCCCCAGAG AGTGAGAAAG GCTCTCTTGA GAGACAGGGA AGTTGCCATC	720
20	CTCAGTAAAA AACTTGCAAC TCTGGTGACG AACGCACCTG TTGAAGTGGA CTGGGAAGAG	780
	ATGAAATACA GAGGATACGA CAAGAGAAAA CTACTTCCGA TATTGAAAGA ACTGGAGITT	840
	GCTTCCATCA TGAAGGAATC TCAACTGTAC GAAGAAGCAG AACCACCCGG ATACGAAATC	900
	GTGAAGGATC ATAAGACCTT CGAAGATCTC ATCGAAAAGC TGAAGGAGGT TCCATCTTTT	960
	GCCCTGGACC TTGAACAGTC CTCCCTTGAC CCGTTCAACT GTGAGATAGT CGGCATCTCC	1020
25	GTGTCGTTC AACCAGAAAC AGCTTATTAC ATTCCACTTC ATCAGAGAAA CGCCAGAAAT	1080
	CTTGATGAAA CACTGGTGCT GTCGAAGTTG AAAGAGATCC TCGAAGACCC GTCTTCGAAG	1140
	ATTGTGGGTC AGAAGCTGAA GTACGACTAC AAGGTTCTTA TGGTAAAGGG TATATCGCCA	1200
	GTTTATCCGC ATTTTGACAC GATGATAGCT GCATATTGTC TGGAGCCAAA CGAGAAAAAA	1260
	TTCAATCTCG AAGATCTGTC TTTGAAATTT CTCGGATACA AAATGACGTC TTATCAGGAA	1320

	CTGATGTCGT TTTCCTCACC ACITTTTGGT TTCAGCTTTG CGGATGTTCC GGTAGACAAG	1380
	GCTCGGAAT ACTCCTGCGA GGATGCAGAC ATCACTTATA GGCTCTACAA GATACTCAGC	1440
	ATGAAGCTCC ATGAAGCGGA ACTTGAGAAC GTCTTCTACA GGATAGAGAT GCCGTTGGTG	1500
	AACGTTCTTG CACGCATGGA ATTGAACGGG GTGTATGTGG ACACAGAATT CCTGAAAAAG	1560
5	CTCTCGGAGG AGTACGGCAA AAAGCTCGAG GAACTGGCCG AAAAAATCTA CCAGATAGCA	1620
	GGTGAGCCCT TCAACATCAA TTCTCCAAAA CAGGTTTCAA AGATCCTTTT TGAGAAGCTG	1680
	GGAATAAAAC CCCGTGGAAA AACGACAAAA ACAGGAGAGT ACTCTACCAG GATAGAGGTG	1740
	TTGGAAGAGA TAGCGAATGA GCACGAGATA GTACCCCTCA TTCTCGAGTA CAGAAAGATC	1800
	CAGAACTGA AATCGACCTA CATAGACACC CTTCCGAAAC TTGTGAACCC GAAACCGGA	1860
10	AGAATTCTATG CATCTTTCCA CCAGACGGGT ACCGCCACTG GCAGGTTGAG TAGCAGTGAT	1920
	CCAAATCTTC AGAATCTTCC GACAAAGAGC GAAGAGGGAA AAGAAATTAG AAAAGCGATT	1980
	GTGCCCCAGG ATCCAGACTG GTGGATCGTC AGTGCGGATT ATTCCCAAT AGAACTCAGA	2040
	ATCTCTCGTC ATCTCAGTGG TGATGAGAAC CTTGTGAAGG CCTTCGAGGA GGCATCGAT	2100
	GTGCACACCT TGATGCCTC CAGGATCTAC AACGTAAAGC CAGAAGAAGT GAACGAAGAA	2160
15	ATGCGACGGG TTGGAAGAT GGTGAACTTC TCTATAATAT ACGGTGTCAC ACCGTACGGT	2220
	CTTTCTGTGA GACTTGGAAT ACCGTTTAA GAAGCAGAAA AGATGATTAT CAGCTATTTC	2280
	ACACTGTATC CAAAGGTGCG AAGCTACATC CAGCAGGTTG TTGCAGAGGC AAAAGAGAAG	2340
	GGCTACGTCA GGACTCTCTT TGGAAGAAAA AGAGATATTC CCCAGCTCAT GGCAAGGGAC	2400
	AAGAACACCC AGTCCGAAGG CGAAAGAATC GCAATAAACA CCCCCATTCA GGAACGGCG	2460
20	GCAGATATAA TAAAAATTGGC TATGATAGAT ATAGACGAGG AGCTGAGAAA AAGAAACATG	2520
	AAATCCAGAA TGATCATTC A GGTTCATGAC GAACTGGTCT TCGAGGTTCC CGATGAGGAA	2580
	AAAGAAGAAC TAGTTGATCT GGTGAAGAAC AAAATGACAA ATGTGGTGAA ACTCTCTGTG	2640
	CCTCTTGAGG TTGACATAAG CATCGAAAA AGCTGGTCTT GA	2682

(2) INFORMATION FOR SEQ ID NO:2:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

000133.052701

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
35 40 45

10 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
85 90 95

15 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
115 120 125

20 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
165 170 175

25 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
195 200 205

30 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270
 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285
 5 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300
 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320
 10 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335
 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350
 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365
 15 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400
 20 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415
 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445
 25 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480
 30 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495
 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525
 35 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu

00891332-562701

	545				550					555					560
	Gly	Ile	Lys	Pro	Arg 565	Gly	Lys	Thr	Thr	Lys 570	Thr	Gly	Glu	Tyr	Ser Thr 575
5	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val Pro 590
	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr Tyr Ile 605	
	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly Arg 620	Ile	His Ala	
10	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu Ser Ser Ser 635	Asp	640	
	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu Gly Lys Glu Ile 650	655		
15	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp Trp Ile Val Ser Ala 660	670			
	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala His Leu Ser Gly Asp 675	685			
	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly Ile Asp Val His Thr Leu 690	700				
20	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu	Glu Val Asn Glu Glu 705	720		
	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn Phe Ser Ile Ile Tyr Gly Val 725	730	735				
25	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly Ile Pro Val Lys Glu Ala 740	745	750			
	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu Tyr Pro Lys Val Arg Ser 755	760	765			
	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys Glu Lys Gly Tyr Val Arg 770	775	780			
30	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro Gln Leu Met Ala Arg Asp 785	790	795	800		
	Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg	Ile Ala Ile Asn Thr Pro Ile 805	810	815			
35	Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala Met Ile Asp Ile Asp 820	825	830		
	Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys	Ser	Arg Met Ile Ile Gln Val 835	840	845		

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880

5 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 Met Ser Leu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu
1 5 10 15

Leu Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu
20 25 30

20 Val Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg
35 40 45

Gly Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe
50 55 60

Ala Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr
65 70 75 80

25 Gly Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu
85 90 95

Lys Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser
100 105 110

30 Leu Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys
115 120 125

Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn
130 135 140

Leu Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp
145 150 155 160

Pro Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val
165 170 175

Leu Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met
180 185 190

5 Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu
195 200 205

Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu
210 215 220

10 Leu Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val
225 230 235 240

Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr
245 250 255

Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu
260 265 270

15 Glu Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala
275 280 285

Arg Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys
290 295 300

20 Leu Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile
305 310 315 320

Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val
325 330 335

Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr
340 345 350

25 Thr Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile
355 360 365

Ala Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile
370 375 380

30 Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn
385 390 395 400

Pro Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala
405 410 415

Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr
420 425 430

35 Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp
435 440 445

Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg

	450	455	460
	Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu		
	465	470	475 480
5	Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val		
		485	490 495
	Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val		
		500	505 510
	Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg		
		515	520 525
10	Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe		
		530	535 540
	Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu		
		545	550 555 560
15	Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp		
		565	570 575
	Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu		
		580	585 590
	Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile		
		595	600 605
20	Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met		
		610	615 620
	Lys Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val		
		625	630 635 640
25	Pro Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met		
		645	650 655
	Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile		
		660	665 670
	Gly Lys Ser Trp Ser		
		675	

30 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 610 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- 35
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Lys	Glu	Leu	Gln	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	
	1				5						10				15		
5	Ile	Val	Lys	Asp	His	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	
				20					25					30			
	Glu	Val	Pro	Ser	Phe	Ala	Leu	Ala	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	
				35				40					45				
	Phe	Asn	Cys	Glu	Ile	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	
		50					55					60					
10	Ala	Tyr	Tyr	Ile	Pro	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	
	65					70					75				80		
	Thr	Leu	Val	Leu	Ser	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	
					85					90					95		
15	Lys	Ile	Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	
				100					105					110			
	Lys	Gly	Ile	Ser	Pro	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	
			115						120				125				
	Tyr	Leu	Leu	Glu	Pro	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	
		130					135					140					
20	Leu	Lys	Phe	Leu	Gly	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	
						150					155				160		
	Phe	Ser	Ser	Pro	Leu	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	
					165					170					175		
25	Lys	Ala	Ala	Asn	Tyr	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	
				180					185					190			
	Tyr	Lys	Ile	Leu	Ser	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	
			195					200					205				
	Phe	Tyr	Arg	Ile	Glu	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	
			210				215					220					
30	Leu	Asn	Gly	Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	
		225				230					235				240		
	Glu	Tyr	Gly	Lys	Lys	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	
					245					250					255		
35	Ala	Gly	Glu	Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	
				260					265					270			
	Leu	Phe	Glu	Lys	Leu	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	

	275							280							285						
	Gly	Glu	Tyr	Ser	Thr	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu					
	290						295					300									
5	His	Glu	Ile	Val	Pro	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu					
	305					310					315					320					
	Lys	Ser	Thr	Tyr	Ile	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr					
					325					330					335						
	Gly	Arg	Ile	His	Ala	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg					
				340					345					350							
10	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu					
			355					360					365								
	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp					
		370					375					380									
15	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala					
	385					390					395					400					
	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile					
				405						410					415						
	Asp	Val	His	Thr	Leu	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu					
				420					425					430							
20	Glu	Val	Asn	Glu	Glu	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser					
			435					440					445								
	Ile	Ile	Tyr	Gly	Val	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile					
		450					455					460									
25	Pro	Val	Lys	Glu	Ala	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr					
	465					470					475					480					
	Pro	Lys	Val	Arg	Ser	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu					
					485					490					495						
30	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln					
				500					505					510							
	Leu	Met	Ala	Arg	Asp	Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg	Ile	Ala					
			515					520					525								
	Ile	Asn	Thr	Pro	Ile	Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala					
		530					535					540									
35	Met	Ile	Asp	Ile	Asp	Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys	Ser	Arg					
	545					550					555					560					
	Met	Ile	Ile	Gln	Val	His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Glu					

	565		570		575
	Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val				
	580		585		590
5	Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser				
	595		600		605
	Trp Ser				
	610				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Met Asn Ser Ser Ser Val Pro Ile Pro Gly Val Thr Gly Ile Gly Glu	
	1	15
	Lys Thr Ala Val Gln Leu Leu Gly Lys Tyr Arg Asn Leu Glu Tyr Ile	
	20	30
20	Leu Glu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu Leu	
	35	45
	Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu Val	
	50	60
25	Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg Gly	
	65	80
	Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe Ala	
	85	95
	Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly	
	100	110
30	Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys	
	115	125
	Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu	
	130	140
	Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro	

	145		150		155		160
	Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu						
		165			170		175
5	Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro						
		180			185		190
	Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu						
		195		200		205	
	Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile						
		210		215		220	
10	Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp						
		225		230		235	240
	Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu						
			245		250		255
15	Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro						
		260		265			270
	Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr						
		275		280		285	
	Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu						
		290		295		300	
20	Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg						
		305		310		315	320
	Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu						
		325		330			335
25	Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr						
		340		345			350
	Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser						
		355		360		365	
	Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr						
		370		375		380	
30	Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala						
		385		390		395	400
	Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln						
		405		410			415
35	Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro						
		420		425		430	
	Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr						

	435	440	445
	Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys 450 455 460		
5	Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro 465 470 475 480		
	Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile 485 490 495		
	Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu 500 505 510		
10	Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys 515 520 525		
	Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn 530 535 540		
15	Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu 545 550 555 560		
	Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr 565 570 575		
	Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala 580 585 590		
20	Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile 595 600 605		
	Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg 610 615 620		
25	Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys 625 630 635 640		
	Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys 645 650 655		
	Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro 660 665 670		
30	Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr 675 680 685		
	Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly 690 695 700		
35	Lys Ser Trp Ser 705		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125

Met Arg Phe Ser Leu Ile Thr Gly Ala Lys Asp Met Leu Gln Leu Val
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240
 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255
 5 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270
 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285
 10 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300
 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320
 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335
 15 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350
 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365
 20 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400
 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415
 25 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445
 30 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480
 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495
 35 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510

Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525
 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540
 5 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu
 545 550 555 560
 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
 565 570 575
 10 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
 580 585 590
 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
 595 600 605
 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala
 610 615 620
 15 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
 625 630 635 640
 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
 645 650 655
 20 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 660 665 670
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 675 680 685
 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
 690 695 700
 25 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
 705 710 715 720
 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
 725 730 735
 30 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
 740 745 750
 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
 755 760 765
 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 770 775 780
 35 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
 785 790 795 800

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Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815

Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
820 825 830

5 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
835 840 845

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
850 855 860

10 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

(2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 893 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Leu Phe Leu Phe Ala Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
20 25 30

25 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
35 40 45

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
50 55 60

30 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
100 105 110

35 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu

	115	120	125
	Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val 130 135 140		
5	Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu 145 150 155 160		
	Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro 165 170 175		
	His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn 180 185 190		
10	Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu 195 200 205		
	Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu 210 215 220		
15	Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile 225 230 235 240		
	Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val 245 250 255		
	Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu 260 265 270		
20	Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln 275 280 285		
	Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His 290 295 300		
25	Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe 305 310 315 320		
	Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile 325 330 335		
	Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro 340 345 350		
30	Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser 355 360 365		
	Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln 370 375 380		
35	Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro 385 390 395 400		
	Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro 405 410 415		

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
725 730 735

5 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
755 760 765

10 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815

15 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
835 840 845

20 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 893 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15

00001-00001

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30
 Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45
 5 His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60
 Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80
 10 Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95
 Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110
 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125
 15 Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
 130 135 140
 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160
 20 Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175
 His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190
 Ile Pro Asp Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205
 25 Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220
 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240
 30 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255
 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270
 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285
 35 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300

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Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320
 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335
 5 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350
 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365
 10 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400
 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415
 15 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430
 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445
 20 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480
 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495
 25 Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525
 30 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu
 545 550 555 560
 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
 565 570 575
 35 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
 580 585 590

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	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile
	595							600					605			
	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala
	610						615					620				
5	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp
	625					630					635					640
	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile
					645					650					655	
10	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala
				660					665					670		
	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp
				675				680					685			
	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu
				690			695					700				
15	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu	Glu	Val	Asn	Glu	Glu
					710						715					720
	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val
				725						730					735	
20	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile	Pro	Val	Lys	Glu	Ala
				740					745					750		
	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser
			755					760					765			
	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg
				770			775					780				
25	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp
						790					795					800
	Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg	Ile	Ala	Ile	Asn	Thr	Pro	Ile
					805					810					815	
30	Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala	Met	Ile	Asp	Ile	Asp
				820					825					830		
	Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys	Ser	Arg	Met	Ile	Ile	Gln	Val
				835				840					845			
	His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Glu	Glu	Lys	Glu	Glu	Leu
				850			855					860				
35	Val	Asp	Leu	Val	Lys	Asn	Lys	Met	Thr	Asn	Val	Val	Lys	Leu	Ser	Val
						870					875					880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15
Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
20 25 30
Asn Ala Val Tyr Asp Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
35 40 45
His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
50 55 60
Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
65 70 75 80
Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
85 90 95
Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
100 105 110
Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
115 120 125
Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
130 135 140
Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
145 150 155 160
Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
165 170 175
His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
180 185 190
Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
195 200 205

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220
 Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
 225 230 235 240
 5 Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
 245 250 255
 Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
 260 265 270
 10 Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
 275 280 285
 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
 290 295 300
 Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
 305 310 315 320
 15 Ala Leu Ala Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
 325 330 335
 Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
 340 345 350
 20 Leu His His Arg Asn Ala Gln Asn Leu Asp Glu Thr Leu Val Leu Ser
 355 360 365
 Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
 370 375 380
 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
 385 390 395 400
 25 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
 405 410 415
 Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
 420 425 430
 30 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
 435 440 445
 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Asn Tyr
 450 455 460
 Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
 465 470 475 480
 35 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
 485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Leu Asn Gly Val Tyr
 500 505 510
 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
 515 520 525
 5 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
 530 535 540
 Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile Leu Phe Glu Lys Leu
 545 550 555 560
 10 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Glu Tyr Ser Thr
 565 570 575
 Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
 580 585 590
 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile
 595 600 605
 15 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Ile His Ala
 610 615 620
 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
 625 630 635 640
 20 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
 645 650 655
 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 660 665 670
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 675 680 685
 25 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
 690 695 700
 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
 705 710 715 720
 30 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
 725 730 735
 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
 740 745 750
 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
 755 760 765
 35 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 770 775 780

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Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815

5 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
835 840 845

10 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

15 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu
1 5 10 15

25 Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys
20 25 30

Glu Val Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro
35 40 45

30 Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr
50 55 60

Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu Asp Glu
65 70 75 80

Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser
85 90 95

35 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val

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	100	105	110
	Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala 115 120 125		
5	Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser 130 135 140		
	Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser 145 150 155 160		
	Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp 165 170 175		
10	Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu 180 185 190		
	Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu Asn Val 195 200 205		
15	Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg Met Glu 210 215 220		
	Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu 225 230 235 240		
	Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile 245 250 255		
20	Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Lys Ile 260 265 270		
	Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr 275 280 285		
25	Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu 290 295 300		
	His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu 305 310 315 320		
	Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr 325 330 335		
30	Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg 340 345 350		
	Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu 355 360 365		
35	Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp 370 375 380		
	Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala 385 390 395 400		

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile
 405 410 415
 Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu
 420 425 430
 5 Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser
 435 440 445
 Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Asn Ile
 450 455 460
 10 Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr
 465 470 475
 Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu
 485 490 495
 Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln
 500 505 510
 15 Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala
 515 520 525
 Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala
 530 535 540
 20 Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg
 545 550 555 560
 Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu
 565 570 575
 Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val
 580 585 590
 25 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser
 595 600 605
 Trp Ser
 610

(2) INFORMATION FOR SEQ ID NO:11:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /note= "'Xaa' is any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Arg Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Xaa Tyr Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Asp Asn Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gln Ala Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Val Phe Ala Phe Thr Glu Thr Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Pro Val Ala Phe Asp Ser Glu Thr Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ile Val Ser Asp Ile Glu Ala Asn Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACGTTTCAA GCGCTAGGGC AAAAGA

26

(2) INFORMATION FOR SEQ ID NO:23:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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GTATATTATA GAGTAGITAA CCATCTTTCC A

31

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Phe Leu Phe Asp Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Leu Val Asp Gly His
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Leu Ile Thr Gly Asp Lys Asp Met Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAGGCCAGG GCTGTGCCCG CAAAGAGAAA TAGTC

35

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAAGCATATC CTGGCGCCG GITATTATGA AAATC

35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCAGACGG GTACCGCCAC TGGCAGGTTG

30

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TATAGAGTAG TTAACCATCT TTCCAACCCG TTTCATTTC TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

25 TATAGAGTAG TTAACCATCT TTCCAACCCG TTGCATTTC TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTTCATTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:34:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TATAGAGTAG TTAACCATCT TTCCAACCCG ATGCATTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:35:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGATGGTTA ACGCGTCTAT AATATACGG

29

(2) INFORMATION FOR SEQ ID NO:36:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAAGAGGCAC AGAGAGTTTC ACC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATTATA GAGGAGTTAA CCATCTTTCC

30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGATGGTTA ACTTCTCTAT AATATACGG

29

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTACATGTCT TCGTTCAC

48

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TATAGAGTAG TTAACCATCT TTCCAACCCG CAACATGTCT TCGTTCAC

48

10 (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTGGCCGCC CGATGCATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGGCCGCC CGCTTCATGA GGGGGTCCAC

30

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs

30

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGCCGCC CTGTACATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

15 GTATATTATA GAGGTGTAA CCATCTTCC

30

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGAGACCGG AATTCTCCTT CATTAAATCC TATA

34

25 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

30

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGAGACCCT GGAACATATAG GAATTAATGA AGGAGAATTC CGGTCTCCC

49

(2) INFORMATION FOR SEQ ID NO:47:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTATTTTGGT ATGCTTGTGC

20

(2) INFORMATION FOR SEQ ID NO:48:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTATTTTGGG ATATATGTGC CT

22

(2) INFORMATION FOR SEQ ID NO:49:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ACGAACATTG TACAAGTTAC

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTTCAGAGAA ACTGACCTGT

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATAAATGCC AAACATGTTG T

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCTCTCAGG ATTTCTCTCA

20

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(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCTTGAGAC CTCTGTCTCC

20

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTGAGAAGA AACAGTGATG GT

22

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGGAGTCGC AAGCTGAAC AGC

23

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCCTGAGTGA CAGAGTGAGA ACC

23

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

15

CCCACTAGGT TGTAACTCC ATGA

24

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TACTATGTGC CAGGCTCTGT CCTA

24

25 (2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTCATGAAG GTGACAGTTC

20

(2) INFORMATION FOR SEQ ID NO:60:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGTTGTGA CCTATTGCAT

20

(2) INFORMATION FOR SEQ ID NO:61:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCTCTGTTC CCTCCCTGTT

20

(2) INFORMATION FOR SEQ ID NO:62:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTATTTGGCC TTGAAGGTAG

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCCCGTGTT GGAACCATGA CTG

23

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TACATAGCGA GACTCCATCT CCC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTATGCGAG CGTATGGATA

20

000133.06201
102290.2221200

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

16

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

16

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CATGAAATGC TGACTGGGTA

20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

15 TCAATTATG TGCAGCCAAT

20

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATAGCGAGA CTCATCTCC

20

25 (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGGAGAGGGC AAAGATCGAT

20

(2) INFORMATION FOR SEQ ID NO:73:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AACACTAGTG ACATTATTTT CA

22

(2) INFORMATION FOR SEQ ID NO:74:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGCTAGGCCT GAAGGCTTCT

20

(2) INFORMATION FOR SEQ ID NO:75:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

102290-2221820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCCTAGTGGG TGATAAGAAT AATC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGACAGATGA TAAATACATA GGATGGATGG

30

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTCTCTTACA AACTGCCCC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATTTGGATGG CTTGACAGAG

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACATTCTAAG ACTTTCCTAA T

21

10 (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGAGCATGCA CCTGAATTG

20

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGAACCATG CGATACGACT

20

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CATTCTCTAGA TGGGTAAAGC

20

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

15 GCTTAGTCAT ACGAGCGG

18

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCCACAGCCA TGTAAGCC

18

25 (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CCCCGGAGCA AGTTCA

16

(2) INFORMATION FOR SEQ ID NO:86:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGCCCAAG CCAGATTA

18

(2) INFORMATION FOR SEQ ID NO:87:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATATGTGAGT CAATCCCCA AG

22

(2) INFORMATION FOR SEQ ID NO:88:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10001332-002701

TGTATTAGTC AATGTTCTCC AG

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAGCTGCCCT AGTCAGCAC

19

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTCCGAGT GCAGGTCACA

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATTCTGGGCG CACAAGAGTG A

21

20

33

- GAAGTTCACC ATCCGGCCGA CCCGTCGCAT TTC